

# SEQUENCE LISTING

<110> Pausch, Mark H  
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816,011

<141> 1997-03-11

<150> 08/332,312

<151> 1994-10-31

<150> PCT/US95/14364

<151> 1995-10-25

<160> 67

<170> PatentIn Ver. 2.1

<210> 1

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<213> Drosophila melanogaster

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 Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu  
 35 40 45  
 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu  
 50 55 60  
 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro  
 65 70 75 80  
 Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe  
 85 90 95

Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser  
 100 105 110  
 Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile  
 115 120 125  
 Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe  
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 Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met  
 145 150 155 160  
 Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr  
 165 170 175  
 Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro  
 180 185 190  
 Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser  
 195 200 205  
 Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp Tyr  
 210 215 220  
 Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe  
 225 230 235 240  
 Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly  
 245 250 255  
 Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys  
 260 265 270  
 Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr  
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 Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg  
 290 295 300  
 Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr  
 305 310 315 320  
 Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp  
 325 330 335  
 Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg  
 340 345 350

Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly  
355 360 365

Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu  
370 375 380

Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu  
385 390 395 400

Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu  
405 410 415

Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser  
420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr  
435 440 445

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu  
450 455 460

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu  
465 470 475 480

Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln  
485 490 495

Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met  
500 505 510

Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His  
515 520 525

Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp  
530 535 540

Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala  
545 550 555 560

Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro  
565 570 575

Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val  
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Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg  
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<212> PRT  
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Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn  
35 40 45  
Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser  
50 55 60  
Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly

65					70					75						80
Lys	Phe	Leu	Ser	Glu	His	Leu	Val	Trp	Leu	Tyr	Gly	Asn	Tyr	Leu	Lys	
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Leu	Lys	Tyr	Leu	Ile	Leu	Ser	Arg	His	Arg	Lys	Glu	Arg	Arg	Glu	His	
			100					105					110			
Val	Cys	Glu	His	Cys	His	Ser	His	Gly	Met	Gly	His	Asp	Met	Asn	Ile	
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Glu	Glu	Lys	Arg	Ile	Pro	Ala	Phe	Leu	Val	Leu	Ala	Ile	Leu	Ile	Val	
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Tyr	Thr	Ala	Phe	Gly	Gly	Val	Leu	Met	Ser	Lys	Leu	Glu	Pro	Trp	Ser	
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Leu	Tyr	Ile	Ile	Leu	Gly	Lys	Phe	Ser	Met	Lys	Lys	Lys	Gln	Lys	Phe	
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Lys	Ile	Phe	Leu	Gly	Leu	Ala	Ile	Thr	Thr	Met	Cys	Ile	Asp	Leu	Val	
	210					215					220					
Gly	Val	Gln	Tyr	Ile	Arg	Lys	Ile	His	Tyr	Phe	Gly	Arg	Lys	Ile	Gln	
225					230					235					240	
Asp	Ala	Arg	Ser	Ala	Leu	Ala	Val	Val	Gly	Gly	Lys	Val	Val	Leu	Val	
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Ser	Glu	Leu	Tyr	Ala	Asn	Leu	Met	Gln	Lys	Arg	Ala	Arg	Asn	Met	Ser	
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Arg	Glu	Ala	Phe	Ile	Val	Glu	Asn	Leu	Tyr	Val	Ser	Lys	His	Ile	Ile	
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Pro	Phe	Ile	Pro	Thr	Asp	Ile	Arg	Cys	Ile	Arg	Tyr	Ile	Asp	Gln	Thr	
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 <213> Caenorhabditis elegans

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 <213> Caenorhabditis elegans

<400> 6  
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<210> 7  
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 <213> Drosophila melanogaster

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<210> 9  
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<213> Drosophila melanogaster

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Arg Tyr Ile Thr Asp His Cys Pro  
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<210> 10  
<211> 24  
<212> PRT  
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<400> 10  
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Ile Ser Pro Thr Thr Phe Ala Gly  
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<211> 24  
<212> PRT  
<213> Drosophila melanogaster

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<210> 12  
<211> 24  
<212> PRT  
<213> Drosophila melanogaster

<400> 12  
Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly Tyr Gly Asp



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Met Val Pro Glu Thr Ile Ala Gly  
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&lt;210&gt; 13

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 13

Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly Tyr Gly Asp  
1 5 10 15

Ile Cys Pro Thr Thr Ala Leu Gly  
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&lt;210&gt; 14

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&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 14

Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly Tyr Gly Asp  
1 5 10 15

Met Ala Pro Lys Thr Tyr Ile Gly  
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&lt;210&gt; 15

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 15

Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly Phe Gly Asn  
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&lt;212&gt; PRT

<213> Drosophila melanogaster

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<210> 17

<211> 24

<212> PRT

<213> Drosophila melanogaster

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Tyr Val Pro Thr Phe Gly Ala Asn  
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<210> 18

<211> 24

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<213> Drosophila melanogaster

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Ile Ser Pro Thr Thr Phe Ala Gly  
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<210> 19

<211> 24

<212> PRT

<213> Drosophila melanogaster

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Tyr Val Pro Thr Phe Gly Ala Asn  
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<210> 21  
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<210> 25

<211> 24

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<212> DNA

<213> Drosophila melanogaster

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<210> 30

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<212> DNA

<213> *Drosophila melanogaster*

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27

<210> 31

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<213> *Drosophila melanogaster*

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<210> 36  
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 <212> DNA  
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<210> 37  
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 <213> *Drosophila melanogaster*

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20 25 30

Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu  
35 40 45

Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu  
50 55 60

Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro  
65 70 75 80

Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe  
85 90 95

Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser  
100 105 110

Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile  
115 120 125

Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe  
130 135 140

Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met  
145 150 155 160

Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr  
165 170 175

Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro  
180 185 190

Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser  
195 200 205

Leu Tyr Tyr Ser Tyr Val Thr Ile Thr Thr Ile Gly Phe Gly Asp Tyr  
210 215 220

Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe  
225 230 235 240

Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly  
245 250 255

Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys

260

265

270

Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr  
 275 280 285

Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg  
 290 295 300

Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr  
 305 310 315 320

Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp  
 325 330 335

Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg  
 340 345 350

Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly  
 355 360 365

Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu  
 370 375 380

Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu  
 385 390 395 400

Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu  
 405 410 415

Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser  
 420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr  
 435 440 445

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu  
 450 455 460

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu  
 465 470 475 480

Trp

<210> 38

<211> 337

<212> PRT



<213> Caenorhabditis elegans

<220>

<221> UNSURE

<222> (337)

<223> X AT RESIDUE 337 IS AN UNKNOWN RESIDUE

<400> 38

Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser  
1 5 10 15

Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser  
20 25 30

Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn  
35 40 45

Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser  
50 55 60

Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly  
65 70 75 80

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys  
85 90 95

Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His  
100 105 110

Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile  
115 120 125

Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val  
130 135 140

Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser  
145 150 155 160

Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly  
165 170 175

Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu  
180 185 190

Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe  
195 200 205

Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val

210	215	220
Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln		
225	230	235 240
Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val		
245	250	255
Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser		
260	265	270
Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile		
275	280	285
Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr		
290	295	300
Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln		
305	310	315 320
Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys		
325	330	335

Xaa

<210> 39  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: DEGENERATE  
 PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<220>  
 <221> variation  
 <222> (2)  
 <223> N AT BASE 2 INDICATES ANY NUCLEOTIDE

<400> 39  
 tnggatwygg wgaywyt

17

<210> 40  
 <211> 18  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DEGENERATE  
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<400> 40

rtcwccrwah ccd aydgt

18

<210> 41

<211> 28

<212> DNA

<213> Homo sapiens

<400> 41

cgcaggcaga gccacaaaga gtacacag

28

<210> 42

<211> 26

<212> DNA

<213> Homo sapiens

<400> 42

ggagatcagc taggcacCat atttgg

26

<210> 43

<211> 26

<212> DNA

<213> Homo sapiens

<400> 43

atgctgcatg cctcatgCtt cccagc

26

<210> 44

<211> 20

<212> DNA

<213> Homo sapiens

<400> 44

ggttatttaa agagagggct

20

<210> 45

<211> 426

<212> PRT

<213> Homo sapiens

<400> 45

Met Leu Pro Ser Ala Ser Arg Glu Arg Pro Gly Tyr Arg Ala Gly Val  
1 5 10 15

Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys  
20 25 30

Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val  
35 40 45

Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr  
50 55 60

Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe  
65 70 75 80

Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val  
85 90 95

Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr  
100 105 110

Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly  
115 120 125

Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu  
130 135 140

Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe  
145 150 155 160

Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile Ile  
165 170 175

Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly Val  
180 185 190

Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val Glu  
195 200 205

Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile Ile  
210 215 220

Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala Leu  
225 230 235 240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala  
245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr  
260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val  
275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu  
290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu  
305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val  
325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr  
340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu  
355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu  
370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu  
385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly  
405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys  
420 425

<210> 46

<211> 2130

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (35)

<223> N AT POSITION 35 INDICATES UNDETERMINED  
NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2057)  
 <223> N AT POSITION 2057 INDICATES UNDETERMINED  
 NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2067)  
 <223> N AT POSITION 2067 INDICATES UNDETERMINED  
 NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2111)  
 <223> N AT POSITION 2111 INDICATES UNDETERMINED  
 NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2120)  
 <223> N AT POSITION 2120 INDICATES UNDETERMINED  
 NUCLEOTIDE

<400> 46  
 ccatacctaata acgactcaact atagggetcg agcgnccgcc cgggcagtaa aatgcctgcc 60  
 cgtgcagctc ggagcgcgca gccgtctct gaataagaag tgagtacaat ggcggtgttg 120  
 taacaaaaaag cttcaagtcc gtctttttca aaaaacattt tgaatgctgc atgcctcatg 180  
 cttcccagcg cctcgcggga gagaccggc tatagagcag gaggggcggc acctgacttg 240  
 ctggatccta aatctgcgcgc tcagaactcc aaaccgaggc tctcattttc cacgaaaccc 300  
 acagtgcctt cttcccgggt ggagagtgac acgaccatta atgttatgaa atggaagacg 360  
 gtctccacga tattcctggg ggtgtcctc tatctgatca tcggagccac cgtgttcaaa 420  
 gcattggagc agcctcatga gatttcacag aggaccacca ttgtgatcca gaagcaaaca 480  
 ttcatatccc aacattcctg tgtcaattcg acggagctgg atgaactcat tcagcaaata 540  
 gtggcagcaa taaatgcagg gattataccg ttaggaaaca cctccaatca aatcagtcac 600  
 tgggatttgg gaagttcctt cttctttgct ggcactgtta ttacaacat aggatttggg 660  
 aacatctcac cacgcacaga agcggcaaaa atattctgta tcatctatgc cttactggga 720  
 attcccctct ttgggtttct cttggctgga gttggagatc agctaggcac catatttggg 780  
 aaaggaattg ccaaagtggg agatacgttt attaagtggg atgttagtca gaccaagatt 840  
 cgcatactct caacaatcat atttatacta tttggctgtg tactctttgt ggctctgcct 900  
 gogatcatat tcaaacaacat agaaggtgg agtgccctgg acgccattta ttttgtggtt 960  
 atcactctaa caactattgg atttggtgac tacgttgacg gtggatccga tattgaatat 1020  
 ctggacttct ataagcctgt cgtgtggttc tggatccttg tagggcttgc ttactttgct 1080  
 gctgtcctga gcatgatgg gagattggc cgagtgatat ctaaaaagac aaaagaagag 1140  
 gtgggagagt tcagagcaca cgtgctgag tggacagcca acgtcacagc cgaattcaaa 1200  
 gaaaccagga ggcgactgag tgtggagatt tatgacaagt tccagcgggc cacctccatc 1260  
 aagcggaagc tctcggcaga actggctgga aaccacaatc aggagctgac tccttgtagg 1320

aggaccctgt cagtgaacca cctgaccagc gagagggatg tcttgccctcc cttactgaag 1380  
 actgagagta tctatctgaa tggtttggcg ccacactgtg ctggtgaaga gattgctgtg 1440  
 attgagaaca tcaaatagcc ctctctttaa ataacccttag gcatagccat aggtgaggac 1500  
 ttctctatgc tctttatgac tgttgctggt agcatttttt aaattgtgca tgagctcaaa 1560  
 gggggaacaa aatagataca cccatcatgg tcatctatca tcaagagaat ttggaattct 1620  
 gagccagcac tttctttctg atgatgcttg ttgaacggcc cactttcttt gatgagtgga 1680  
 atgacaagca atgtctgatg cctttgtgtg ccagactgt tttcctctct ctttccctaa 1740  
 tgtgccataa ggcctcagaa tgaattgaga attgtttctg gtaacaatgt agctttgagg 1800  
 gatcagttct taacttttca ggtctacct aactgagcct agatatggac catttatgga 1860  
 tgacaacaat tttttttttg taaatgacaa gaaattctta tgcagccttt tacctaagaa 1920  
 atttctgtca gtgccttata ttatgaagaa acagaacctc tctagctaag gtgtgggttc 1980  
 tcttccctg cccccacccc taggtcacc tctgcagtct tttaccccag ttctccatt 2040  
 tgaataccat accttgntgg aaacagngtg taaaatgact gaagtgatga tgccgaagat 2100  
 gaaatagatg ncaaattagn tggacattga 2130

<210> 47  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 aaaagatcta aaatgcttcc cagcgcc

27

<210> 48  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 aaagtcgacc tatttgatgt tctcaat

27

<210> 49  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 aaaaagctta aaatgcttcc cagcgcc

27

<210> 50  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 50  
aaatctagac tatttgatgt tctcaat

27

<210> 51  
<211> 534  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (262)  
<223> N AT POSITION 262 INDICATES UNDETERMINED  
NUCLEOTIDE

<400> 51  
aacaaaaacc ttttttgttt tgaatggcct agagagggta agggatcccc tgacgaacag 60  
gagcagagcc agctagaacc tgggcctggc cagttcaagg ccaccagagg gcagccttct 120  
gcggaaggca gtattggggg aggcaggac ccacgcagac atggcactca gagctctcac 180  
tgtccactga ctctctcttc tccaggttat ggccacatgg cccactatc gccaggcgga 240  
aaggccttct gcatggtctt antagccctt gggctgccag cctccttagc tctcgtggcc 300  
accctgcgcc attgcctgct gcctgtgctc agccgccccac gtgcctgggt agcgggtccac 360  
tggcagctgt caccggccag ggctgcgctg ctgcaggcag ttgcaactggg actgctggtg 420  
gccagcagct ttgtgctgct gccagcgtg gtgctgtggg gccttcaggg cgactgcagc 480  
ctgctggggg ccgtctactt ctgcttcagc tcgctcagca ccattggcct gggg 534

<210> 52  
<211> 956  
<212> DNA  
<213> Mus musculus

<400> 52  
atgatacgat ttaatacgac tcactatagg gaatttgccc ctcgaggcca agaattcggc 60  
acgaggagaa tgtgcgcacg ttggtctca tcgtgtgcac cttcacctac ctgctggtgg 120  
gcgccgcggt gttcgacgca ctggagtcgg agccggagat gatcgagcgg cagcggctgg 180  
agctgcggca gctggagctg cgggcgcgct acaacctcag cgaggcgggc tacgaggagc 240  
tggagcgcgt cgtgctgcgc ctcaagccgc acaaggccgg cgtgcagtgg cgcttcgccg 300  
gctccttcta cttcgccatc accgtcatca ccaccatcgg ctatggtcac gcggcgccca 360  
gcacggacgg aggcaagggt ttctgcatgt tctacgcgct gctgggcac cgcctcacac 420  
tagtcatgtt ccagagcctg ggtgaacgca tcaacacctc cgtgaggtac ctgctgcacc 480  
gtgccaaagag ggggctgggc atgcggcacg ccgaagtgtc catggccaac atggtgctca 540  
tcggtttcgt gtcgtgcac cgcacgtgt gcatcggcgc agctgccttc tctactacg 600  
agcgtggtac tttcttcacg gctattact actgcttcat caccctcacc accatcggct 660  
tcggcgacta tgtggcgctg cagaaggacc aggcgctgca gacgcagccg cagtatgtgg 720  
cttcagcttc gtgtacatcc tcacgggctc acggtcatcg gcgcttcctc aacctcgtgg 780  
tgctgcgatt catgaccatg aacgccagg acgagaagcg tgatgcggag caccgcgcc 840  
tgctcacgca caacggccag gctgtcggcc tgggtggcct gagctgctg agcggtagcc 900



tgggcgacgg cgtgcgtccc cgcgaccag tcacatgcgc tgcggccgca agctta

956

<210> 53  
<211> 1055  
<212> DNA  
<213> Mus musculus

<220>  
<221> unsure  
<222> (247)  
<223> N AT POSITION 247 INDICATES UNDETERMINED  
NUCLEOTIDE

<220>  
<221> unsure  
<222> (593)  
<223> N AT POSITION 593 INDICATES UNDETERMINED  
NUCLEOTIDE

<220>  
<221> unsure  
<222> (952)  
<223> N AT POSITION 952 INDICATES UNDETERMINED  
NUCLEOTIDE

8' int.  
<400> 53  
ctgaaaccat gggcccgata cctgctcctg cttatggccc acctgctggc catgggcctt 60  
ggggtgtgtg tgcttcaggc cctggagggc cctccagctc gccacctcca ggcccaggtc 120  
caggctgaac tggctagctt ccaggcagag cacagggcct gcttgccacc tgaggccctg 180  
gaggagctgc taggtgcggt cctgagagca caggcccatg gagtttccag cctgggcaac 240  
agctcanaga caagcaactg ggatctgccc tcagctctgc tgttccactgc cagcatcctc 300  
accaccaccg gttatggcca catggcccca ctctcctcag gtggaaaggc cttctgtgtg 360  
gtctatgcag cccttgggct gccagcctct ctagcacttg tggctgccct gcgccactgc 420  
ttgctgcctg tgttcagtcg cccaggtgac tgggtagcca ttcgctggca gctggcacca 480  
gctcaggctg ctctgctaca ggcagcagga ctgggcctcc tgggtggcctg tgtcttcatg 540  
ctgctgccag cactggtgct gtggggtgta cagggtgact ggcagcctgc tanaaccatc 600  
tacttctggt tcggctcact cagcacgac gccctaggag acttgcctgc tgcccattga 660  
cgtggcctgc acccagccat ttaccacctt gggcagtttg cacttcttgg ttacttgctc 720  
ctggggctcc tggccatggt gttagcagta gagaccttct cagagctgcc tcagggtccgt 780  
gccatggtga aattcttttg gccagtggtc tctagaaccg atgaagatca agatggcatc 840  
ctaggccaag atgagctggc tctgagcact gtgctgcctg acgccccagt cttgggacca 900  
accaccccag cctgagcggg aggcaccaag gaggcttga agaacatagc angaagggtt 960  
atgggaatga atatgtcatg ggataatgtt aatttttaaaa attaaatggg ctgcttagca 1020  
tgcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1055

<210> 54

<211> 178  
<212> PRT  
<213> Homo sapiens

<220>  
<221> UNSURE  
<222> (88)  
<223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 54

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser  
1 5 10 15

Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe  
20 25 30

Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly  
35 40 45

Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr  
50 55 60

Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly  
65 70 75 80

Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu  
85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg  
100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala  
115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe  
130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser  
145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly  
165 170 175

Leu Gly

<210> 55

<211> 309

<212> PRT

<213> Mus musculus

<400> 55

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg  
1 5 10 15

Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala  
20 25 30

Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln  
35 40 45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser  
50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro  
65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala  
85 90 95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr  
100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro  
115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser  
130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His  
145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys  
165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg  
180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr  
195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln  
210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala



Ser Ser Xaa Thr Ser Asn Trp Asp Leu Pro Ser Ala Leu Leu Phe Thr  
 85 90 95  
 Ala Ser Ile Leu Thr Thr Thr Gly Tyr Gly His Met Ala Pro Leu Ser  
 100 105 110  
 Ser Gly Gly Lys Ala Phe Cys Val Val Tyr Ala Ala Leu Gly Leu Pro  
 115 120 125  
 Ala Ser Leu Ala Leu Val Ala Ala Leu Arg His Cys Leu Leu Pro Val  
 130 135 140  
 Phe Ser Arg Pro Gly Asp Trp Val Ala Ile Arg Trp Gln Leu Ala Pro  
 145 150 155 160  
 Ala Gln Ala Ala Leu Leu Gln Ala Ala Gly Leu Gly Leu Leu Val Ala  
 165 170 175  
 Cys Val Phe Met Leu Leu Pro Ala Leu Val Leu Trp Gly Val Gln Gly  
 180 185 190  
 Asp Trp Gln Pro Ala Xaa Thr Ile Tyr Phe Cys Phe Gly Ser Leu Ser  
 195 200 205  
 Thr Ile Gly Leu Gly Asp Leu Leu Pro Ala His Gly Arg Gly Leu His  
 210 215 220  
 Pro Ala Ile Tyr His Leu Gly Gln Phe Ala Leu Leu Gly Tyr Leu Leu  
 225 230 235 240  
 Leu Gly Leu Leu Ala Met Leu Leu Ala Val Glu Thr Phe Ser Glu Leu  
 245 250 255  
 Pro Gln Val Arg Ala Met Val Lys Phe Phe Gly Pro Ser Gly Ser Arg  
 260 265 270  
 Thr Asp Glu Asp Gln Asp Gly Ile Leu Gly Gln Asp Glu Leu Ala Leu  
 275 280 285  
 Ser Thr Val Leu Pro Asp Ala Pro Val Leu Gly Pro Thr Thr Pro Ala  
 290 295 300

<210> 57

<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> VARIANT  
<222> (1)..(9)  
<223> X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT  
POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8  
IS Y, F, V, I, M, OR L

<220>  
<223> Description of Artificial Sequence: POTASSIUM ION  
CHANNEL SEQUENCE

<400> 57  
Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly  
1 5

<210> 58  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: POTASSIUM ION  
CHANNEL SEQUENCE

<220>  
<221> VARIANT  
<222> (1)..(8)  
<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,  
S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I,  
V, L, F, OR Y

<400> 58  
Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa  
1 5

<210> 59  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: POTASSIUM ION

# CHANNEL SEQUENCE

<400> 59

Tyr Ala Leu Leu Gly Ile Pro

1

5

<210> 60

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION  
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (6)

<223> X AT POSITION 6 IS M, I, V, L, F, OR Y

<400> 60

Tyr Ala Leu Leu Gly Xaa Pro

1

5

<210> 61.

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (88)

<223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 61

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser

1

5

10

15

Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe

20

25

30

Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly

35

40

45

Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr

50

55

60

Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly  
65 70 75 80

Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu  
85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg  
100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala  
115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe  
130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser  
145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly  
165 170 175

Leu Gly

<210> 62  
<211> 309  
<212> PRT  
<213> Mus musculus

<400> 62

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg  
1 5 10 15

Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala  
20 25 30

Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln  
35 40 45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser  
50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro  
65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala



85

90

95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr  
100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro  
115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser  
130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His  
145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys  
165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg  
180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr  
195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln  
210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala  
225 230 235 240

His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr  
245 250 255

Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu  
260 265 270

Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser  
275 280 285

Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala  
290 295 300

Ala Ala Ala Ser Leu  
305

<210> 63

<211> 434

<212> PRT

<213> Caenorhabditis elegans

<400> 63

Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala  
1 5 10 15

Phe Pro Arg Asp Lys Tyr Asn Ile Val Tyr Trp Leu Val Ile Leu Val  
20 25 30

Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro  
35 40 45

Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp  
50 55 60

Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro  
65 70 75 80

Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro  
85 90 95

Leu Ile Tyr Arg Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu  
100 105 110

Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser  
115 120 125

Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn  
130 135 140

Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly Val Gly Gly Asp  
145 150 155 160

Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys  
165 170 175

Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn  
180 185 190

Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val  
195 200 205

Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp  
210 215 220

Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala  
225 230 235 240

Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn  
245 250 255

Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu  
260 265 270

Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly  
275 280 285

Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu  
290 295 300

Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val  
305 310 315 320

Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile  
325 330 335

Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Phe Cys Asn Tyr Arg  
340 345 350

Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe  
355 360 365

Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala  
370 375 380

Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg  
385 390 395 400

Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr  
405 410 415

Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser  
420 425 430

Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION  
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(7)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,  
S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,  
L, F, OR Y

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro  
1 5

<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence between Ce orfl and Dm orfl

<400> 65

Thr Trp Thr Phe  
1

<210> 66

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus  
sequence between Ce orfl and Dm orfl

<400> 66

Gly Tyr Gly Asn  
1

<210> 67

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus

sequence between Ce orf1 and Dm orf1

<400> 67

Gly Phe Gly Asp

1

Seq  
62

D'  
uncl.